#8

Page: 1

Raw Sequence Listing

07/19/91 16:16:24

1		SEQUENCE LISTING
2		
3	(1) GE	NERAL INFORMATION:
4		
5	(1)	APPLICANT: Carter, Paul J.
6		Presta, Leonard G.
7 8	/225	
9	(11)	TITLE OF INVENTION: Immunoglobulin Variants
10	/:::>	MIMBED OF CEOURNAEC. 10
11	(111)	NUMBER OF SEQUENCES: 10
12	/i=\	CORRESPONDENCE ADDRESS:
13	(14)	(A) ADDRESSEE: Genentech, Inc.
14	•	(B) STREET: 460 Point San Bruno Blvd
15		(C) CITY: South San Francisco
16		(D) STATE: California
17		(E) COUNTRY: USA
18		(F) ZIP: 94080
19		(r) 21r: 74000
20	/w\	COMPUTER READABLE FORM:
21	(*)	(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
22		(B) COMPUTER: IBM PC compatible
23		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
24		(D) SOFTWARE: patin (Genentech)
25		(b) boilmand. patin (denenteen)
26	(vi)	CURRENT APPLICATION DATA:
27	(+-/	(A) APPLICATION NUMBER: 07/715,272
28		(B) FILING DATE: 14-June-1991
29		(C) CLASSIFICATION:
30		(*)
31	(vii)	PRIOR APPLICATION DATA:
32	(,	(A) APPLICATION NUMBER:
33		(B) FILING DATE:
34		(-,
35	(viii)	ATTORNEY/AGENT INFORMATION:
36	(/	(A) NAME: Adler, Carolyn R.
37		(B) REGISTRATION NUMBER: 32,324
38		(C) REFERENCE/DOCKET NUMBER: 709
39)
40	(ix)	TELECOMMUNICATION INFORMATION:
41	\ /	(A) TELEPHONE: 415/266-2614
42	,	(B) TELEFAX: 415/952-9881
43		(C) TELEX: 910/371-7168
44		(-)
45	(2) IN	FORMATION FOR SEQ ID NO:1:
46	` '	
47	(i)	SEQUENCE CHARACTERISTICS:
48	\- /	(A) LENGTH: 109 amino acids
49		(B) TYPE: amino acid
50		(D) TOPOLOGY: linear
51		
52	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1:
53	\ <i>\</i>	

Page: 2

Raw Sequence Listing

07/19/91 16:16:26

54 55 56	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
57 58 59	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ala 25	Ser	Gln	Asp	Val	Asn 30
60 61 62	Thr	Ala	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
63 64 65	Leu	Leu	Ile	Tyr	Ser 50	Ala	Ser	Phe	Leu	Glu 55	Ser	Gly	Val	Pro	Ser 60
66 67 68	Arg	Phe	Ser	Gly	Ser 65	Arg	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
69 70 71	Ser	Ser	Leu	Gln	Pro 80	Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
72 73 74	His	Tyr	Thr	Thr	Pro 95	Pro	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
75 76 77	Ile	Lys	Arg	Thr 109											
78 79	(2)					_									
80	(:	•	_	NCE (.						
81	(:	(1	A) LI	engti	H: 12	20 ar	nino		is						
	(:	(1	_	ENGTI YPE:	H: 12 amir	20 ar	nino cid		is						
81 82	(-	(1	A) LI B) Ti	ENGTI YPE:	H: 12 amir	20 ar	nino cid		ls						
81 82 83 84 85	·	(1 (1	A) LI B) Ti	ENGTI (PE: OPOLO	H: 12 amir DGY:	20 ar 10 ac line	mino cid ear	acio		10 : 2 :	:				
81 82 83 84 85 86	(x:	(1 (1 (1 i.) SI	A) LI B) TY D) T(ENGTI (PE: OPOLO	H: 12 amir DGY: DESCR	20 ar no ac line	mino cid ear	acio SEQ	ID 1						
81 82 83 84 85	(x:	(1 (1 (1 i.) SI	A) LI B) T' D) T(ENGTI (PE: OPOLO	H: 12 amir DGY: DESCR	20 ar no ac line	mino cid ear	acio SEQ	ID 1			Val	Gln	Pro	Gly 15
81 82 83 84 85 86 87 88 89 90	(x: Glu 1	() (I (I) SI Val	A) LI B) TY D) T(ENGTI (PE: DPOL(NCE I	H: 12 amir DGY: DESCR Val 5	20 am 10 ac 1ine RIPTI	nino cid ear ION:	SEQ Gly	ID 1	Gly 10	Leu				15
81 82 83 84 85 86 87 88 90 91 92 93	(x: Glu 1 Gly	(I (I (I Val Val	A) LI B) TY D) TO EQUEN	ENGTI (PE: OPOLO NCE I Leu	H: 12 amir DGY: DESCR Val 5 Leu 20	20 am no ac line RIPT: Glu Ser	nino cid ear ION: Ser	SEQ Gly	ID 1 Gly Ala	Gly 10 Ser 25	Leu Gly	Phe	Asn	Ile	15 Lys 30
81 82 83 84 85 86 87 88 99 99 99 99 99 99 99 99 99	Glu 1 Gly Asp	(1 (1 (1) Si) Ser	A) LI B) TY D) TO EQUEN Gln	ENGTH YPE: DPOLO NCE I Leu Arg	H: 12 Amir DGY: DESCR Val 5 Leu 20 His 35	20 am 10 am 11 m RIPTI Glu Ser	mino cid ear CON: Ser Cys	seQ Gly Ala	ID N Gly Ala Gln	Gly 10 Ser 25 Ala 40	Leu Gly Pro	Phe Gly	Asn Lys	Ile Gly	15 Lys 30 Leu 45
81 82 83 84 85 86 87 88 99 99 99 99 99 99 99 99 99	Glu 1 Gly Asp	(1 (1 i) Si Val Ser Thr	A) LI B) TY C) TO EQUEN Gln Leu Tyr	ENGTI (PE: OPOLO NCE I Leu Arg Ile	H: 12 Amir DGY: DESCR Val 5 Leu 20 His 35 Arg 50	20 am 10 ac 11nc RIPT Glu Ser Trp	mino cid ear ION: Ser Cys Val	SEQ Gly Ala Arg	ID R Gly Ala Gln Thr	Gly 10 Ser 25 Ala 40 Asn 55	Leu Gly Pro Gly	Phe Gly Tyr	Asn Lys Thr	Ile Gly Arg	15 Lys 30 Leu 45 Tyr 60
81 82 83 84 85 86 87 88 99 99 99 99 99 99 99 99 99	Glu 1 Gly Asp Glu Ala	(I (I (I) (I) Val Ser Thr Trp	A) Li B) TY C) TO EQUEN Gln Leu Tyr	ENGTI YPE: OPOLO NCE I Leu Arg Ile Ala Val	H: 12 Amir DGY: DESCR Val 5 Leu 20 His 35 Arg 50 Lys 65	20 am 10 ac 11 nc RIPT Glu Ser Trp Ile Gly	mino cid car ION: Ser Cys Val Tyr Arg	SEQ Gly Ala Arg Pro	ID R Gly Ala Gln Thr	Gly 10 Ser 25 Ala 40 Asn 55 Ile 70	Leu Gly Pro Gly Ser	Phe Gly Tyr Ala	Asn Lys Thr	Ile Gly Arg	15 Lys 30 Leu 45 Tyr 60 Ser 75

107	
108	Ala Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
109	110 115 120
110	
111	
112	(2) INFORMATION FOR SEQ ID NO:3:
113	
114	(i) SEQUENCE CHARACTERISTICS:
115	(A) LENGTH: 109 amino acids
116	(B) TYPE: amino acid
117	(D) TOPOLOGY: linear
118	
119	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
120	
121	Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
122	1 5 10 15
123	
124	Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser
125	20 25 30
126 127	Con Man Tou Blo Man Man Cla Cla T - Bu Cl T - Bu
128	Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
129	35 40 45
130	Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser
131	
132	50 55 60
133	Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
134	65 70 75
135	70 75
136	Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
137	80 85 90
138	
139	Tyr Asn Ser Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
140	95 100 105
141	
142	Ile Lys Arg Thr
143	109
144	
145	(2) INFORMATION FOR SEQ ID NO:4:
146	
147	(i) SEQUENCE CHARACTERISTICS:
148	(A) LENGTH: 120 amino acids
149	(B) TYPE: amino acid
150	(D) TOPOLOGY: linear
151	
152	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
153	
154	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
155	1 5 10 15
156	
157	Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
158	20 25 30
159	

160 161	Asp	Tyr	Ala	Met	Ser 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
162					-					***					~
163	Glu	Trp	Val	Ala	Val	Tle	Ser	Glu	Asn	Glv	Glv	Tur	Thr	Ara	Tur
164					50					55	011	-1-		9	60
165															00
166	Ala	Asp	Ser	Val	Lvs	Glv	Ara	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser
167					65	1	9			70			p		75
168															
169	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Ara	Ala	Glu	Asp
170	_				80					85		-			90
171															
172	Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tvr
173				_	95	-		_	•	100	•	•	•		105
174						,									
175	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
176			_		110	_		_		115					120
177															
178															
179	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:5:							
180															
181	(i) SI	EQUEI	NCE (CHAR	ACTE	RIST	ICS:							
182		(2	A) LI	ENGTI	H: 10)9 aı	nino	acio	ds						
183		(1	B) T	YPE:	amiı	ao a	cid								
184		. (1	D) T(OPOL	OGY:	line	ear.								
185													•		
186	(x	i) SI	EQUE	NCE I	DESCI	RIPT	ION:	SEQ	ID 1	NO: 5	:				
187															
188	Asp	Ile	Val	Met	Thr	Gln	Ser	His	Lys	Phe	Met	Ser	Thr	Ser	Val
189	1				5					10					15
190						•									
191	Gly	Asp	Arg	Val	Ser	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Asn
192					20		•			25					30
193															
194	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	His	Ser	Pro	Lys
195					35				•	40					45
196													•		
197	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Phe	Arg	Tyr	Thr	Gly	Val	Pro	Asp
198					50					55					60
199															
200	Arg	Phe	Thr	Gly	Asn	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile
201					65					70					75
202															
203	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	Tyr	Cys	Gln	Gln
204					80					85					90
205															
206	His	Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu
207					95					100					105
208															
209	Ile	Lys	Arg										•		
210				109											
211 212	(2)														

112														
213 214	/25	CROTTE	TOP (711 R D 1	s amm	. T. C. C.								
21 4 215	(1)	SEQUE						. _						
215 216		(A) LI					acı	15						
		(B) T												
217		(D) T	OPOLO	JGY:	line	ear								
218		0501								_				
219	(X1)	SEQUE	NCE I	DESCI	RIPT.	ION:	SEQ	ID I	NO: 6	:				
220 221	G1 W	-1 (1)-	T	a1	61		61	D	~1	•	77 3	T	D	~ 1-
221 222		al Gln	Leu		GIN	ser	GTÅ	Pro		Leu	VAI	rys	Pro	_
223	1			5					10					15
223 224	710 C	om Tou	T 0	T 0	C	C	mb	710	C	61	Dha	B ===	71.	T
225	NIG 3	er Leu	ry s	20	Set	Cys	THE	ALA	25	GIY	PHE	ASII	116	30
226				20					23					30
227	Aco T	hr Tyr	Tla	wie	Twn	17-1	T	Cln	N	Dwo	61	61 n	61	T 01
228	rsb I	mr tår	116	35	пр	VAI	пÃр	GIII	40	PIU	GIU	GIII	GIY	45
229				33					40					-
230	Glu T	rp Ile	Glv	Ara	Tle	Tur	Pro	Thr	Acn	Glv	Tur	ጥኪሎ	Ara	Tur
231		- P	1	50		-1-			55	1	-1-		••• 9	60
232									-					•
233	Asp P	ro Lys	Phe	Gln	Asp	Lvs	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser
234				65		-1-			70			-		75
235														
236	Ser A	sn Thr	Ala	Tvr	Leu	Gln	Val	Ser	Ara	Leu	Thr	Ser	Glu	Ast
237				80					85					90
238									-					
239	Thr A	la Val	Tvr	Tvr	Cvs	Ser	Arq	Trp	Glv	Glv	Asp	Glv	Phe	Tvr
240			•	95	- 4		3		100	2		4		105
241														
242	Ala M	et Asp	Tyr	Trp	Gly	Gln	Gly	Ala	Ser	Val	Thr	Val	Ser	Ser
243			_	110	_		_		115					120
244														
245														
246	(2) IN	FORMAT	ION F	FOR S	SEQ :	ID NO	0:7:							
47														
248	(i)	SEQUE	NCE C	CHAR	ACTE	RIST:	ICS:							
249		(A) LI	ENGTI	1: 27	7 bas	ses								
250		(B) T	YPE:	nuc	leic	acio	d							
51		(C) S				•	gle							
52		(D) T	OPOLO	GY:	line	ear								
53					•									
54	(xi)	SEQUE	ICE I	DESCI	RIPT	ON:	SEQ	ID I	NO: 7	:				
55														
56														
57		TCCGAT	CATCO	CAG	CTGA	CCCA	GTC	CCA	27					
58														
59														
60														
61	(2) IN	FORMAT	ON F	FOR S	SEQ :	ID NO	3:8:							
62	_													
63	(i)	SEQUE					ICS:							
64		(A) LI					_							
265		(R) TY	PE:	nucl	leic	acid	4							

Page: 6

Raw Sequence Listing

07/19/91 16:16:34

266	(C) STRANDEDNESS: single
267	(D) TOPOLOGY: linear
268	
269	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
270	·
271	
272	GTTTGATCTC CAGCTTGGTA CCHSCDCCGA A 31
273	
274	
275	
276	(2) INFORMATION FOR SEQ ID NO:9:
277	(-)
278	(i) SEQUENCE CHARACTERISTICS:
279	(A) LENGTH: 22 bases
280	(B) TYPE: nucleic acid
281	(C) STRANDEDNESS: single
282	(D) TOPOLOGY: linear
283	(b) for obodi. Timear
284	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
285	(x1) bigoinch biscriftion. big is no. 7.
286	
287	AGGTSMARCT GCAGSAGTCW GG 22
288	AGGISMARCI GCAGSAGICW GG 22
289	
290	
291	(2) INFORMATION FOR SEQ ID NO:10:
292	(2) INFORMATION FOR SEQ ID NO:10:
293	(i) SEQUENCE CHARACTERISTICS:
294	(A) LENGTH: 34 bases
295	
296	(B) TYPE: nucleic acid
297	(C) STRANDEDNESS: single (D) TOPOLOGY: linear
298	(D) TOPOLOGY: Timear
298 299	(wi) GROVENOR BEGGETTEROW, GRO IN WO. 10.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
300	
301	
302	TGAGGAGACG GTGACCGTGG TCCCTTGGCC CCAG 34
303	
304	

PAGE: 1

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/715,272A

DATE: 07/19/91 TIME: 16:16:36

LINE ERROR

ORIGINAL TEXT

27 Wrong application Serial Number

(A) APPLICATION NUMBER: 07/715,272

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/07/715,272A

MANDATORY IDENTIFIER THAT WAS NOT FOUND

DATE: 07/19/91 TIME: 16:16:36

PAGE: 1

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/07/715,272A

CORRECTED TEXT

DATE: 07/19/91 TIME: 16:16:36

LINE ORIGINAL TEXT